

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2001, 19:13:06 ; Search time 2802.37 seconds

(without alignments)  
23323.767 Million cell updates/sec

File: US-08-153-397A-1

Sequence: 1 CGGCGCTGAGACTGGGCTCA.....AAAAAAAAACCGGAATTC 3962

Scoring table: IDENTITY\_NUC 1  
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

GenEmbl: 1: gb\_da: 2: gb\_hlg: 3: gb\_in: 4: gb\_om: 5: gb\_ov: 6: gb\_pat: 7: gb\_ph: 8: gb\_pl: 9: gb\_pr: 10: gb\_ro: 11: gb\_sts: 12: gb\_sy: 13: gb\_un: 14: gb\_vl: 15: em\_da: 16: em\_fun: 17: em\_hum: 18: em\_in: 19: em\_om: 20: em\_ov: 21: em\_ov: 22: em\_pat: 23: em\_ph: 24: em\_pl: 25: em\_ro: 26: em\_sts: 27: em\_sy: 28: em\_un: 29: em\_vl: 30: em\_hlgo\_hum: 31: em\_hlgo\_inv: 32: em\_hlgo\_rnd: 33: em\_hlg\_hum: 34: em\_hlg\_inv: 35: em\_hlg\_rnd: 36: em\_hlg\_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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#### ALIGNMENTS

RESULT 1  
LOCUS I68738 168738 3962 bp DNA  
DEFINITION Sequence 1 from patent US 5677144.  
ACCESSION I68738  
VERSION I68738.1 GI:2830860  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3962)  
AUTHORS Dillrich, A. and Alves, F. Hildagard Elisabeth.  
TITLE Recombinant DNA encoding CCK 2, a receptor tyrosine kinase  
JOURNAL Patent: US 5677144-A 1 14-OCT-1997;  
FEATURES  
source 1. 3962  
BASE COUNT 735 a 1234 c 1182 g 811 t  
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Query Match 100.0%; Score 3962; DB 6; Length 3962;  
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Matches 3962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 REFERENCE 1 (bases 1 to 3738)  
 AUTHORS Johnson, J.D., Edman, J.C. and Rutter, W.J.  
 TITLE A receptor tyrosine kinase found in breast carcinoma cells has an extracellular discoidin I-like domain  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)  
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 AUTHORS Strausberg, R.  
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 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
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 CONTACT: MGC help desk  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
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 Zhang, L.-H. and Green, E.D.  
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DEFINITION Homo sapiens tyrosine protein kinase (CAK) gene, complete cds.
ACCESSION L20817

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VERSION L20817.1 GI:306474
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Perez,J.L., Shen,X., Finkernagel,S., Sclorria,L., Jenkins,N.A.,
Gilbert,D.J., Copeland,N.G. and Wong,T.W.
Identification and chromosomal mapping of a receptor tyrosine
kinase with a putative phospholipid binding sequence in its
ectodomain
Oncogene 9, 211-219 (1994)
MEDLINE 94134417
REFERENCE 2 (bases 1 to 3803)
AUTHORS Johnson,J.D.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1993) J.D. Johnson
REFERENCE 3 (sites)
AUTHORS Johnson,J.D., Edman,J.C. and Rutter,W.J.
TITLE A receptor tyrosine kinase found in breast carcinoma cells has an
extracellular discoidin I-like domain
Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)
JOURNAL 93296201
MEDLINE 4 (sites)
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QY 1630 TGGCTGGCGGGTGGAGCTGGGAGGAGGCTCTGAGAGGCTGAGAGGAGGCTGGAG 1689
Db 1502 TGGCTGGCGGGTGGAGCTGGGAGGAGGCTCTGAGAGGCTGAGAGGAGGCTGGAG 1561
QY 1690 AGGAGCTGACGGTTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1749
Db 1562 AGGAGCTGACGGTTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621
QY 1750 GTCTAGAGAGCAACCCCGTACAGAGAGCCCGGCTGCTGAGGAGTCCGCCCACTCG 1809
Db 1622 GTCTAGAGAGCAACCCCGTACAGAGAGCCCGGCTGCTGAGGAGTCCGCCCACTCG 1681
QY 1810 CTCCCTGTGTCCCAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1869
Db 1682 CTCCCTGTGTCCCAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
QY 1870 TGGCACTTACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1929
Db 1742 TGGCACTTACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801
QY 1930 CCACAACACCCAGAGCTTACAGTGGGACTATATGAGAGCTGAGAGGCAAGGAGCCCGC 1989
Db 1802 CCACAACACCCAGAGCTTACAGTGGGACTATATGAGAGCTGAGAGGCAAGGAGCCCGC 1861
QY 1990 TTTTGGCCCCCAGCTTCCCAAGACAGCTCCCATATATGCCAGGCTGACATTTTACC 2049
Db 1862 TTTTGGCCCCCAGCTTCCCAAGACAGCTCCCATATATATGCGAGGCTGACATTTTACC 1921
QY 2050 TGCAGGGCGTACCGGGGGGCAACACATATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2109
Db 1922 TGCAGGGCGTACCGGGGGGCAACACATATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1981
QY 2110 GGGATGGCCCCCGAGATGATTTCCCTGATCTCAGACTCCGCTTCAAGAGAAAGCTTG 2169
Db 1982 GGGATGGCCCCCGAGATGATTTCCCTGATCTCAGACTCCGCTTCAAGAGAAAGCTTG 2041
QY 2170 GCGAGGGCCAGTTTGGGAGAGTGCACCTGTGTGAGGTGCAAGAGCTCAAGATCTGGTCA 2229
Db 2042 GCGAGGGCCAGTTTGGGAGAGTGCACCTGTGTGAGGTGCAAGAGCTCAAGATCTGGTCA 2101
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QY	2230	GTCTGATTTCCCTCCCTTAATGTGGTAAAGGACACCTTTCGCTGGAGCTGCACGATCT	2289
Db	2102	GTCTTGATTTCCCTCCCTTAATGTGGTAAAGGACACCTTTCGCTGGAGCTGCACGATCT	2161
QY	2290	TACGGCCAGATGCCACCAAGAATGCCAGCTTCTCTGTCTCCAGGAATGATTTCTCGTA	2349
Db	2162	TACGGCCAGATGCCACCAAGAATG-----CCAGGAATGATTTCTCGTA	2203
QY	2350	AAGAGGTAAATATCATGTCCAGGCTCAAGACCCCAACATCATTTGGCTGTGGCCGTGT	2409
Db	2204	AAGAGGTAAATATCATGTCCAGGCTCAAGAGCCCAACATCATTTGGCTGTGGCCGTGT	2263
QY	2410	GTGTCCAGAGGACCCCTCGATGTATTCATCATACATGGAGAAAGCCGACCTCAAC	2463
Db	2264	GTGTCCAGAGGACCCCTCGATGTATTCATCATACATGGAGAAAGCCGACCTCAAC	2323
QY	2470	AGTTCCATAGTCCCAACAGCTGGAAGACAGGACCCAGAGGGGCCCTCGGAGCGGGC	2539
Db	2324	AGTTCCATAGTCCCAACAGCTGGAAGACAGGACCCAGAGGGGCCCTCGGAGCGGGC	2383
QY	2530	AGGCTGGCCAGGGGCCCAACATCAGCTACCCAACTGCTGCATGTGGACGCCAGATCG	2589
Db	2384	AGGCTGGCCAGGGGCCCAACATCAGCTACCCAACTGCTGCATGTGGAGCCCGAGATCG	2443
QY	2580	CCTCCGGCATCGGTATCTCGGCCCACTCAACTTTTACATGGGAGCCGTGGCACGCGGA	2649
Db	2444	CCTCCGGCATCGGTATCTCGGCCCACTCAACTTTTACATGGGAGCCGTGGCACGCGGA	2503
QY	2650	ACTGCTAGTTGGGAAATTTACCATCAATAATCCAGACTTTTGGCATAGACCGGAAC	2709
Db	2504	ACTGCTAGTTGGGAAATTTACCATCAATAATCCAGACTTTTGGCATAGACCGGAAC	2563
QY	2710	TCTATGCTGGGGACATTTACCCTGTGTGACAGGGCCGGCAGTCTGCCATCGCTGGATGG	2769
Db	2564	TCTATGCTGGGGACATTTACCCTGTGTGACAGGGCCGGCAGTCTGCCATCGCTGGATGG	2623
QY	2770	CCTGGAGATGATCTCATATGGGGAAGTCAACGATCGAGTACAGTGGAGGCGCTTGGTG	2829
Db	2624	CCTGGAGATGATCTCATATGGGGAAGTCAACGATCGAGTACAGTGGAGGCGCTTGGTG	2683
QY	2830	TGACCTGTGGGAGGTCTGATCTCTGTAAAGGCCAGCCCTTTGGGAGAGCTCAACGAG	2889
Db	2684	TGACCTGTGGGAGGTCTGATCTCTGTAAAGGCCAGCCCTTTGGGAGAGCTCAACGAG	2743
QY	2880	AGCAGGTATCGAGAACGCGGGGGAATTCTTCCGGGACCAAGGGCCGCGAGGTACTGT	2949
Db	2744	AGCAGGTATCGAGAACGCGGGGGAATTCTTCCGGGACCAAGGGCCGCGAGGTACTGT	2803
QY	2950	CCGGCCGGCCGCTGTGCCGAGGGGCTTAATAGATGATGTTGGGTGTGAGACCGGG	3009
Db	2804	CCGGCCGGCCGCTGTGCCGAGGGGCTTAATAGATGATGTTGGGTGTGAGACCGGG	2863
QY	3010	AGTCTGAGACAGCGACCCCTTTTCCACATCGATCGGTCTCTGGCAAGAGTGCATCA	3069
Db	2864	AGTCTGAGACAGCGACCCCTTTTCCACATCGATCGGTCTCTGGCAAGAGTGCATCA	2923
QY	3070	ACACGGTGTGAATCACAATCGAGTGGCCCTCCCTCAGGAGTGTACAGGGGAAGCA	3129
Db	2924	ACACGGTGTGAATCACAATCGAGTGGCCCTCCCTCAGGAGTGTACAGGGGAAGCA	2983
QY	3130	GTGACATATAAACAAGAGACAAATAGGACACTGTGCGCTTCCCTCCGACAGCCATC	3189
Db	2984	GTGACATATAAACAAGAGACAAATAGGACACTGTGCGCTTCCCTCCGACAGCCATC	3043
QY	3190	ACCTCTAATAGAGGACGTGAGTGGAGTGGGCTGGGGCCCAACCAAGGAGCTATGGCC	3249
Db	3044	ACCTCTAATAGAGGACGTGAGTGGAGTGGGCTGGGGCCCAACCAAGGAGCTATGGCC	3098
QY	3250	CTTCTCCCTTCTCTGGACACACTCTCATGTCCCTTCTCTGTCTTCTCTCTAGAACCC	3309
Db	3099	CTTCTCCCTTCTCTGGACACACTCTCATGTCCCTTCTCTGTCTTCTCTCTAGAACCC	3158
QY	3310	CTGTGCGCCACCAAGTGGTCTGTGTGATGGATCTCTCCACACCTCTCTAGCAATCC	3369

[illegible][illegible]

Query Match	87.1%	Score 3451;	DB 6;	Length 3637;
Best Local Similarity	97.0%	Pred. No. 0;		
Matches 3589;	Conservative	0;	Mismatches 5;	Indels 105;
			Gaps	3.
Qy	256	GTGGACTTGAAGCAATCCCAAGAGATGCTGCCCCCCTTAGGCCCGAGGATCAG	315	
	17	GTGGACTTGAAGGATCCCAAGAGATGCTGCCCCCCTTAGGCCCGAGGATCAG	76	

QY	316	GGCTATGAGACCAAGAGCCCTGTCACTTTTAACTGCTGCTGCTCTTGGTGGCAATGGAG	375
Db	77	GAGCTATGAGGACCAAGAGCCCTGTCACTTTTAACTGCTGCTGCTCTTGGTGGCAATGGAG	136
QY	376	ATGCTGACATAAGGAGACATTTTAACTCGGCAATGGCCGATATCCCTGGGCAATGGAG	435
Db	137	ATGCTGACATBAAGGAGACATTTTAACTCGGCAATGGCCGATATCCCTGGGCAATGGAG	196
QY	436	ACCGGACCATCCAGACAGTACATCTCTGCTCCAGCTCCGTGTCAGATTCCATCTGGCG	495
Db	197	ACCGGACCATCCAGAGAGTACATCTCTGCTCCAGCTCCGTGTCAGATTCCATCTGGCG	256
QY	496	CCCGCCACAGAGTGTGAGAGCAAGTACGGGATGGGGCTGTGCCCCCGAGGGTGG	555
Db	257	CCCGCCACAGAGTGTGAGAGCAAGTACGGGATGGGGCTGTGCCCCCGAGGGTGG	316
QY	556	TGTTTCCCAAGGAGAGAGTACTTGCAAGTGGATCTCAACGATCTCACTGTGTGCTC	615
Db	317	TGTTTCCCAAGGAGAGAGTACTTGCAAGTGGATCTCAACGATCTCACTGTGTGCTC	376
QY	616	TGTTGGGACCCAGAGAGCGGATCCGGGGGCTTGGGCAAGAGTTCCTCCGAGCTACC	675
Db	377	TGTTGGGACCCAGAGAGCGGATCCGGGGGCTTGGGCAAGAGTTCCTCCGAGCTACC	436
QY	676	GGCTGCTTACTCCCGGATGTGTGCGCGCTGGATGGGCTGGAAAGACCGTGGGGTCAAG	735
Db	437	GGCTGCTTACTCCCGGATGTGTGCGCGCTGGATGGGCTGGAAAGACCGTGGGGTCAAG	496
QY	736	AGGATCTCAGGCAATGAGGAGCCCTGAGGAGTGTGCTAAAGGACTTGGGCCCCCA	795
Db	497	AGGATCTCAGGCAATGAGGAGCCCTGAGGAGTGTGCTAAAGGACTTGGGCCCCCA	556
QY	796	TGTTTGGCCGACTGTTGCTTACCCCGGGCTGACCGGGTATGAGTGTGCTGTGCG	855
Db	557	TGTTTGGCCGACTGTTGCTTACCCCGGGCTGACCGGGTATGAGTGTGCTGTGCG	616
QY	856	GGGTAGAGCTTATGGCTGCTCTGAGAGGATGAGACTCTGTCTTACACCGCCCTGTGG	915
Db	617	GGGTAGAGCTTATGGCTGCTCTGAGAGGATGAGACTCTGTCTTACACCGCCCTGTGG	676
QY	916	GGGAGCAATGTATTTATCTGAGGGCCGTAACTCAACGAACTCCACCTATACGGACTA	975
Db	677	GGGAGCAATGTATTTATCTGAGGGCCGTAACTCAACGAACTCCACCTATACGGACTA	736
QY	976	CCGTGGGCGGACTGACATATGGGGTGTGGGCGACGTGCGAGTGTGTGTTGGGGCTGG	1035
Db	737	CCGTGGGCGGACTGACATATGGGGTGTGGGCGACGTGCGAGTGTGTGTTGGGGCTGG	796
QY	1036	ATGACTTTAGGAAGTCAAGAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGA	1095
Db	797	ATGACTTTAGGAAGTCAAGAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGA	856
QY	1096	GCAACACAGACTCTCCAGTGGGATGTGGAGATGGAGTTTGAATTGTGACCGGCTGAGGG	1155
Db	857	GCAACACAGACTCTCCAGTGGGATGTGGAGATGGAGTTTGAATTGTGACCGGCTGAGGG	916
QY	1156	CCTTCCAGGCTATGAGAGTCCACTGTAAACAATGACACGCTGGAGACCCTGTGCGCT	1215
Db	917	CCTTCCAGGCTATGAGAGTCCACTGTAAACAATGACACGCTGGAGACCCTGTGCGCT	976
QY	1216	GGGGGTGGAATGCTCGCTTCGCGGCTGGCCCTGCGCATGGCTGGGAGGGGAGGCCATGC	1275
Db	977	GGGGGTGGAATGCTCGCTTCGCGGCTGGCCCTGCGCATGGCTGGGAGGGGAGGCCATGC	1036
QY	1276	GGCACAACCTAGGGGGCAACCTTGGGGAGACCCGAGCGCGGGCTGTCAAGTGGCCCTTG	1335
Db	1037	GGCACAACCTAGGGGGCAACCTTGGGGAGACCCGAGCGCGGGCTGTCAAGTGGCCCTTG	1096
QY	1336	GGGGCGGTGTGGCTCGCTTCTCTCAGTGGCGCTTCCCTTTGGCGGGCCGTGTACTCT	1395
Db	1097	GGGGCGGTGTGGCTCGCTTCTCTCAGTGGCGCTTCCCTTTGGCGGGCCGTGTACTCT	1156
QY	1396	TCAGGCAAAATCTCTTCACTCTGATGTGTTGAACAATCTCTCCGGCACTGGAGACA	1455

Db	1157	TCAGCGAAATCTCTCATCTCTATGTGTGGTGAACATTTCTCTCCGGCACTGGAGGCA	1211
QY	1456	CCCTCCCGCCAGACCCCCTGGTGTGGCCGCGCTGGCCACCTCCCAACATTCAGACGCTTGG	1511
Db	1217	CCCTCCCGCCAGACCCCCTGGTGTGGCCGCGCTGGCCACCTCCCAACATTCAGACGCTTGG	1271
QY	1516	AGCTGAGCGCCAGAGGCCAGCAAGCCCGTGGGCAAGGCCGAGGGGAGCCGACCGCATCC	1571
Db	1277	AGCTGAGCGCCAGAGGCCAGCAAGCCCGTGGGCAAGGCCGAGGGGAGCCGACCGCATCC	1331
QY	1576	TCATCGGCGCTGGTGTGGCCATCATCCGCTCGCTGGTGTGCATCATCATTTGGCCCTATGCTCT	1631
Db	1337	TCATCGGCGCTGGTGTGGCCATCATCCGCTCGCTGGTGTGCATCATCATTTGGCCCTATGCTCT	1391
QY	1636	GGCGGCTGCATGGCGCAGGCTCCTCAGCAAGGCTGAAACGAGAGGCTTTGGAAGAGAGC	1691
Db	1397	GGCGGCTGCATGGCGCAGGCTCCTCAGCAAGGCTGAAACGAGAGGCTTTGGAAGAGAGC	1451
QY	1696	TCACGCTTCACCTCTCTCTCTCCCTGGGAGCACTATCTCATCAACACCGCCACGGTCTTA	1751
Db	1457	TCACGCTTCACCTCTCTCTCTCCCTGGGAGCACTATCTCATCAACACCGCCACGGTCTTA	1511
QY	1756	GAGAGCGACCCCCGACAGAGAGCCCGGCGCTGTGGGATTCGGCCCACTCGCTCCCT	1811
Db	1517	GAGAGCGACCCCCGACAGAGAGCCCGGCGCTGTGGGATTCGGCCCACTCGCTCCCT	1571
QY	1816	GTGTCCCAATGGCTCTGTGCTGTCTCATCCAGGCTACCGCTCTCTTTGAGCA	1871
Db	1577	GTGTCCCAATGGCTCTGTGCTGTCTCATCCAGGCTACCGCTCTCTTTGAGCA	1631
QY	1876	CTTTACGCCGCTCCCTCTGAGAGCCCGGAGCCCCCAACACCGCGCTGGGCCAAACCCACA	1931
Db	1637	CTTTACGCCGCTCCCTCTGAGAGCCCGGAGCCCCCAACACCGCGCTGGGCCAAACCCACA	1691
QY	1936	AACACCAGGCGCTAAGTGGGGAGCTATATGGAAGCTGAGAAAGCCAGGCGCCCGCTTCTGC	1991
Db	1697	AACACCAGGCGCTAAGTGGGGAGCTATATGGAAGCTGAGAAAGCCAGGCGCCCGCTTCTGC	1751
QY	1996	CCCCACCTCCCAAGAACAGCTCCCCCATTAATGCGAGAGCTGCATTTGTATTACCTGCAGAG	2051
Db	1757	CCCCACCTCCCAAGAACAGCTCCCCCATTAATGCGAGAGCTGCATTTGTATTACCTGCAGAG	1811
QY	2056	GGCTACCGGGGGGCAACACTATGCTGTGCTGCATGCCCCCAGGGGAGCAATCGGGGATG	2111
Db	1817	GGCTACCGGGGGGCAACACTATGCTGTGCTGCATGCCCCCAGGGGAGCAATCGGGGATG	1871
QY	2116	GGCCCCCAAGATGGATTTCCCTGATCTGTGACTCGGCTTCAAGGAGAACTTGGCGAGG	2171
Db	1877	GGCCCCCAAGATGGATTTCCCTGATCTGTGACTCGGCTTCAAGGAGAACTTGGCGAGG	1931
QY	2176	GCGATTTGGGAGAGTGACACTGTGTAGGTGCAAGCCCTCAAGATCGGTCACTTGTG	2231
Db	1937	GCGATTTGGGAGAGTGACACTGTGTAGGTGCAAGCCCTCAAGATCGGTCACTTGTG	1991
QY	2236	ATTTCCCCCTTAATGTGCGTAAGGGACACCTTGTGTGTAGTGTGCAAGATCTTACGCG	2291
Db	1997	ATTTCCCCCTTAATGTGCGTAAGGGACACCTTGTGTGTAGTGTGCAAGATCTTACGCG	2051
QY	2296	CAGATGCCACCAAAATGCCAGCTTCTCTGTTCACAGAAATGATTTCTGAAAGAGG	2351
Db	2057	CAGATGCCACCAAAATGCCAGCTTCTCTGTTCACAGAAATGATTTCTGAAAGAGG	2081
QY	2356	TGAAGATCATGTGAGGCTCAAGGACCCCAATCATCTTGGCGGTGGGCGGTGTGTGCG	2411
Db	2099	TGAAGATCATGTGAGGCTCAAGGACCCCAATCATCTTGGCGGTGGGCGGTGTGTGCG	2151
QY	2416	AGGAGACCCCCCTGTGCATGATTACTGACTACATGAGAGAAGCGGCACTCAACCAAGTTCC	2471
Db	2159	AGGAGACCCCCCTGTGCATGATTACTGACTACATGAGAGAAGCGGCACTCAACCAAGTTCC	2211
QY	2476	TCAGTCCCAACAGCTGTGAGAGCAAGGCAAGCGAGGGGCGCCCTGGGAGCGGCGAGCTG	2531

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Db 2219 TCAGTGGCCACACAGCTGGAGAGACAGCCGAGGGGCCCTGGGAGCGGAGGCTG 2278
QY 2536 CGAGGGGGCCACACATAGCTACCCAACTGCTGCTGATGTGGAGAGCCCAATGCTCCG 2585
Db 2279 CGAGGGGGCCACACATAGCTACCCAACTGCTGCTGATGTGGAGAGCCCAATGCTCCG 2338
QY 2596 GCATGCGCTATCTGCGCACACTCACTTTGTACATCGGGAGCTGGCCAGCGGAACTGCC 2655
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QY 2656 TAGTGGGGAAAAATTCACCATCAAAATCGACAGCTTTGGCATGAGCGGAACTCTATG 2715
Db 2399 TAGTGGGGAAAAATTCACCATCAAAATCGACAGCTTTGGCATGAGCGGAACTCTATG 2458
QY 2716 CTGGGAGCTATTCACCTGTGTGACAGCGCGGAGCTGCTGCCAATCGCTGATGCTGGG 2775
Db 2459 CTGGGAGCTATTCACCTGTGTGACAGCGCGGAGCTGCTGCCAATCGCTGATGCTGGG 2518
QY 2776 AGTGCATCCCATGGGGAGTTGACAGTGTGACAGCTGGGCTTGGTGTGACCC 2835
Db 2519 AGTGCATCCCATGGGGAGTTGACAGTGTGACAGCTGGGCTTGGTGTGACCC 2578
QY 2836 TGTGGAGAGTGTGATGCTGTGTGAGGGCCAGCCCTTTGGGAGCTCACCCAGAGAGG 2895
Db 2579 TGTGGAGAGTGTGATGCTGTGTGAGGGCCAGCCCTTTGGGAGCTCACCCAGAGAGG 2638
QY 2896 TCATCGAAGACGGGGGAGTTCTCCGGAGCAGGGCCGAGGTGTACCTGTCCGCG 2955
Db 2639 TCATCGAAGACGGGGGAGTTCTCCGGAGCAGGGCCGAGGTGTACCTGTCCGCG 2698
QY 2956 CGCTGCTGCGCCGCGAGGCGCTATGAGCTGTGCTTGGTGTGTGAGCGCGGAGTCTG 3015
Db 2699 CGCTGCTGCGCCGCGAGGCGCTATGAGCTGTGCTTGGTGTGTGAGCGCGGAGTCTG 2758
QY 3016 AGCAGCGACACCCCTTTCCAGCTGATGCTGTGCTGTGAGAGAGTGTACCTGACAGG 3075
Db 2759 AGCAGCGACACCCCTTTCCAGCTGATGCTGTGCTGTGAGAGAGTGTACCTGACAGG 2818
QY 3076 TGTGAATCAACATCCAGTGTCCCTCCCTCAGGAGTATCCAGGGGAGAGCCAGTACA 3135
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QY 3136 CTTAAACAGAGAGACATGAGCTGTGCTGCTTCCCTCCCGAGAGCCCATCAGCTCT 3195
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QY 3196 AATAGAGCAGTGAAGCTCAGGTGGGCTGGGCGCACCGAGGAGTGTATGCCCTTCTC 3255
Db 2939 AATAGAGCAGTGAAGCTC----- 2958
QY 3256 CCTTCTGTGACACTCTCATGTCCCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3315
Db 2959 -----AGAAAGCCCTGTGCG 2972
QY 3316 CCCACCCAGCTGTGCTGTGATGGGATCTCTCCACCTCTCTTACCATCCCTTGGGG 3375
Db 2973 CCCACCCAGCTGTGCTGTGATGGGATCTCTCTCCACCTCTCTTACCATCCCTTGGGG 3032
QY 3376 AAGGCTGGGGAGAAATATATGATAGACATGAGCATGGCCATTTGGAGAGCTGGGCCCC 3435
Db 3033 AAGGCTGGGGAGAAATATATGATAGACATGAGCATGGCCATTTGGAGAGCTGGGCCCC 3092
QY 3436 ACTGGAACAACACTGATTCCTGTGAGAGGTGCTGCG-CCCCAGCTTCTCTCTCTGTAC 3494
Db 3093 ACTGGAACAACACTGATTCCTGTGAGAGGTGCTGCGCCCCAGCTTCTCTCTCTGTAC 3152
QY 3495 ACACGGAGCCCACTGGCGGAGAAATCTGGGGGTGAGAGGAGAAAGAGAGAGAAATG 3554
Db 3153 ACACGGAGCCCACTGGCGGAGAAATCTGGGGGTGAGAGGAGAAAGAGAGAGAAATG 3212
QY 3555 TTTCCTTGTGCTGCTGTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3614
Db 3213 TTTCCTTGTGCTGCTGTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3272

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QY 3615 GAAACACTGGAACCTGGGGGTAGCCCCGCCAGCCCTCAGTACCCCACTTCCCACTTG 3674
Db 3273 GAAACACTGGAACCTGGGGGTAGCCCCGCCAGCCCTCAGTACCCCACTTCCCACTTG 3332
QY 3675 CAGCTTGTAGCTGGAACCTCTCTAGCCTATAGCTTCTGTGTGAGAGTAAATATGGGATT 3734
Db 3333 CAGCTTGTAGCTGGAACCTCTCTAGCCTATAGCTTCTGTGTGAGAGTAAATATGGGATT 3392
QY 3735 GGGGGGAAAGAGGAGCAGAGCCCATAGCTTGGGGGTGAGACATCTCTAGTGTAGCTGC 3794
Db 3393 GGGGGGAAAGAGGAGCAGAGCCCATAGCTTGGGGGTGAGACATCTCTAGTGTAGCTGC 3452
QY 3795 CACATTGATTTTCTATATATCTGCTGCTTGTGACATTTTGGGGGAGAGACACAGAT 3854
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Db 3573 ATATATAAGGTGAGTTTCCACAAAAA 3611

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AR103004
LOCUS AR103004 3637 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6087144.
ACCESSION AR103004
VERSION AR103004.1 GI:12814592
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3637)
AUTHORS Scadden,D.T., Baker,K.P. and Baron,W.F.
TITLE Protein Tyrosine Kinases
JOURNAL Patent: US 6087144-A 3 11-JUL-2000;
FEATURES
source
1..3637
BASE COUNT 721 a 1094 c 1079 g 743 t
ORIGIN

Query Match 87.1%; Score 3451; DB 6; Length 3637;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;

QY 256 GTTGGACTGGAAGAAATGCCAAGATGCTGCCCCACCCCTTAAAGCCCGAGGGATCAG 315
Db 17 GTTGGACTGGAAGAAATGCCAAGATGCTGCCCCACCCCTTAAAGCCCGAGGGATCAG 76
QY 316 GAGCTATGGGAGCAGAGAGCCCTGTCACTTACTGCGTGTCTTGTGGGAGAGTGGAG 375
Db 77 GAGCTATGGGAGCAGAGAGCCCTGTCACTTACTGCGTGTCTTGTGGGAGAGTGGAG 136
QY 376 ATGCTGACATGAAGGAGCAATTTGATCTGCGCAAGTGCAGTATGCCCTGGGATGCAG 435
Db 137 ATGCTGACATGAAGGAGCAATTTGATCTGCGCAAGTGCAGTATGCCCTGGGATGCAG 196
QY 436 ACCGGACATCCCAAGACATGACATCTGCTTCAAGTCTCTGCTGCTGCTGCTGCTGCTG 495
Db 197 ACCGGACATCCCAAGACATGACATCTGCTTCAAGTCTCTGCTGCTGCTGCTGCTGCTG 256
QY 496 CCCGCGACAGAGGTTGAGAGCAGTGTAGGAGGAGTGTAGGAGGAGGAGTGTAGGAGGAG 555
Db 257 CCCGCGACAGAGGTTGAGAGCAGTGTAGGAGGAGTGTAGGAGGAGGAGTGTAGGAGGAG 316
QY 556 TTTTCCCAAGAGAGAGTACTGAGGTGATTTACAGACTTCACCTGCTGCTGCTGCTGCTGCT 615

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Db 317 TGTTCACAGAGAGAGAGTACTTGCAGTGTGATCTAACAGACTGCACCTGCTGGCTC 376  
QY 616 TGTGGGACACCCAGGAGGAGCATGCCGGGGGSCCTGGGGAAGAAGTCTCCCGGAGCTAC 675  
Db 377 TGTGGGACACCCAGGAGGAGGAGCATGCCGGGGGSCCTGGGGAAGAAGTCTCCCGGAGCTAC 436  
QY 676 GGTCTGCTTACTCCCGGAGATGTGCGCGCTGTGATGGCTTGGAAGGACCGTGGGGTCAAG 735  
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QY 736 AGGTGATCTAGGCAATGAGAGACCTTAGGGAGTGTGCTGTAAGAACCTTGGGCCCCCA 795  
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QY 976 CGGTGGGCGGACGTGAGTATAGGGGGTCTGGCCACGCTGGCAGATGCTGTGGGGCTGC 1035  
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QY 1036 ATGACTTTAGGAAGAGTACAGAGCTGGGGGTGGCCAGGCTATGACTATGTGGGATGA 1095  
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QY 1096 GCAACACAGCTTCTCAGTGGCTATGTGAGATGAGAGTTGAGCTTGGACCGGCTGAGG 1155  
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REFERENCE 1 (bases 1 to 3637)  
AUTHORS Godowski, P.J., Mark, M.R. and Scadden, D.T.  
TITLE Nucleic acids encoding protein tyrosine kinases  
JOURNAL Patent: US 6096527-A 3 01-AUG-2000;  
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REFERENCE 1 (bases 1 to 3637)
AUTHORS Godowski, P. J., Mark, M. R. and Scadden, D. T.
TITLE Antibodies specific for Rse receptor protein tyrosine kinase
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 REFERENCE 1 (bases 1 to 3554)  
 AUTHORS Di Marco, E., Cutuli, N., Guerra, L., Cancedda, R. and De Luca, M.  
 TITLE Molecular cloning of trkE, a novel trk-related putative tyrosine  
 kinase receptor isolated from normal human keratinocytes and widely  
 expressed by normal human tissues  
 JOURNAL J. Biol. Chem. 268 (32), 24290-24295 (1993)  
 MEDLINE 94033265  
 REFERENCE 2 (bases 1 to 3554)  
 AUTHORS De Luca, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-SEP-1993) M. De Luca, Istituto Nazionale per la  
 Ricerca sul Cancro, Lab Differenziamento Cellulare, Viale  
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RESULT 11

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 VERSION 229093.1 GI:732799  
 KEYWORDS receptor tyrosine kinase.  
 SOURCE human.

ORGANISM Homo sapiens  
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 REFERENCE 1 (bases 1 to 3841)  
 Laval,S., Butler,R., Shelling,A.N., Hanby,A.M., Poulsen,R. and  
 Ganesan,T.S.  
 TITLE Isolation and characterization of an epithelial-specific receptor  
 tyrosine kinase from an ovarian cancer cell line  
 JOURNAL Cell Growth Differ. 5 (11), 1173-1183 (1994)  
 MEDLINE 95151638  
 REFERENCE 2 (bases 1 to 3841)  
 Shelling,A.N., Butler,R., Jones,T., Laval,S., Boyle,J.M. and  
 Ganesan,T.S.  
 TITLE Localization of an epithelial-specific receptor kinase (EDDR1) to  
 chromosome 6q16  
 JOURNAL Genomics 25 (2), 584-587 (1995)  
 MEDLINE 95309932  
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 Kedinget,C.  
 TITLE Direct Submition  
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 polyA\_site 3828  
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 ORIGIN

Query Match 85.0% Score 3366: DB 9: Length 3841;  
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## RESULT 12

## LOCUS

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 VERSION L57508.1 GI:1160924  
 KEYWORDS receptor kinase.  
 SOURCE Homo sapiens lung cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 3692)  
 Perez,J.L., Jing,S.Q. and Wong,T.W.  
 Identification of two isoforms of the Cak receptor kinase that are  
 coexpressed in breast tumor cell lines  
 JOURNAL OF CELLULAR PHYSIOLOGY 12 (7), 1469-1477 (1996)  
 MEDLINE 96204002

## FEATURES

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QY	2230	GTCCTGATTTCCCTTAAATGTGCGTAAGGGACACCCTTGGTGTAGCTGTCAAGATCT	2289
Pb	1991	GTCCTGATTTCCCTTAAATGTGCGTAAGGGACACCCTTGGTGTAGCTGTCAAGATCT	2050
QY	2290	TACGGCCGAGTGCACCAAAATGCCAGCTTCTCTTGTTCACAGAAATTTCTCGA	2349
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QY	2350	AAGAGTGAAGATCATGTGCAAGCTCAAGGACCCCAATCATTTGGCGGTGGGGCGGT	2409
Db	2093	AAGAGTGAAGATCATGTGCAAGCTCAAGGACCCCAATCATTTGGCGGTGGGGCGGT	2152
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QY	2710	TCTATGCTGGGGGACTATTACCGTGTCAAGGGCCGGGAGTGTGCCATCCGCTGGATGG	2769
Db	2453	TCTATGCTGGGGGACTATTACCGTGTGTACCGTGTGTCAAGGGCCGGGAGTGTGCCATCCGCTGGATGG	2512
QY	2770	CTTGGAGTGCATCTCATATGGGGAAATTCACGACTGCGAGTGTGCTGTGGCTTTGGTG	2829
Db	2513	CTTGGAGTGCATCTCATATGGGGAAATTCACGACTGCGAGTGTGCTGTGGCTTTGGTG	2572
QY	2830	TGACCCCTGTGGGAGGTGTCTGTGTGTAAGGCCACCCCTTTGGCAGTCAACGACG	2889
Db	2573	TGACCCCTGTGGGAGGTGTCTGTGTGTAAGGCCACCCCTTTGGCAGTCAACGACG	2632
QY	2890	AGCAGGTGCATCGAAGAGGGGGGGAGTTCTTCCGGGAGCAGGGCCGGAGGTGTACTGT	2949
Db	2633	AGCAGGTGCATCGAAGAGGGGGGGAGTTCTTCCGGGAGCAGGGCCGGAGGTGTACTGT	2692
QY	2950	CCCGGCCGCTGCTCCCTCCCGCAGGGGCTTATATGACCTATCTTCGAGTGTGAGCGGGG	3009
Db	2693	CCCGGCCGCTGCTCCCTCCCGCAGGGGCTTATATGACCTATCTTCGAGTGTGAGCGGGG	2752
QY	3010	AGTGTAGAGCAGGACACCCCTTTTCCACAGTGCATCGGTGTCTGTGGCAGAGATGCATCA	3069
Db	2753	AGTGTAGAGCAGGACACCCCTTTTCCACAGTGCATCGGTGTCTGTGGCAGAGATGCATCA	2812
QY	3070	ACAGGGGTGAATCAACATCCAGTGGCCCTTCCAGGGAGTGAATTCAGGGGAGGCCA	3129
Db	2813	ACAGGGGTGAATCAACATCCAGTGGCCCTTCCAGGGAGTGAATTCAGGGGAGGCCA	2872
QY	3130	GTCAGACTAAACACAGAGACACATGACACTGTGCCCTTCCCTCCGACAGCCCATC	3189
Db	2873	GTCAGACTAAACACAGAGACACATGACACTGTGCCCTTCCCTCCGACAGCCCATC	2932

QY	3150	ACCTCTAATTAAGAGGAGAGACATGCAAGGAGGGGCTGGGGCCACCCAGGAGAGCTGATGCC	3249
Db	2933	ACCTCTAATTAAGAGGAGAGACATGCAAGGAGGGGCTGGGG-----CAAGGAGAGCTGATGCC	2987
QY	3250	CTTCTCCCTTCCTGCGGACACACTCTCATATGCCCTTCTCTCTCTCTCTCTGAAAGGCC	3309
Db	2988	CTTCTCCCTTCCTGCGGACACACTCTCATATGCCCTTCTCTCTCTCTCTCTGAAAGGCC	3047
QY	3310	CTGTGGCCACCCAGCTGTGTCTGTGGATGGATCTCTCCACCCCTCTCTAGCCATCCC	3369
Db	3048	CTGTGGCCACCCAGCTGTGTCTGTGGATGGATGGATCTCTCCACCCCTCTCTAGCCATCCC	3107
QY	3370	TTGGGGAAGGGTGGGGGAAATATATAGATATAGACACTGAGATGGCCCATTTGAGCACTTG	3429
Db	3108	TTGGGGAAGGGTGGGGGAAATATATAGATATAGACACTGAGATGGCCCATTTGAGCACTTG	3167
QY	3430	GGCCCCACTGGACAACACTGATTCCTGGAAGGGGTGGGCCCAAGCTTCTCTCCCT	3489
Db	3168	GGCCCCACTGGACAACACTGATTCCTGGAAGGGGTGGGCCCAAGCTTCTCTCCCT	3222
QY	3490	GTCACACACTGGAGCCCACTGGCTGAGAAATCTGGGGGTGAGAGGACAAGAAAGAGAGA	3549
Db	3223	GTCACACACTGGAGCCCACTGGCTGAGAAATCTGGGGGTGAGAGGACAAGAAAGAGAGA	3282
QY	3550	AAATGTTTCTCTGTGTGCTGCTCTCTGATCTGTCTCTCAAGCTTGGGCTTCTCTCTCAT	3609
Db	3283	AAATGTTTCTCTGTGTGCTGCTCTCTGATCTGTCTCTCAAGCTTGGGCTTCTCTCTCAT	3342
QY	3610	CACCTGAAACACTGGACCTGGGGGTAGCCCCGCCAGCCCTAGTCACCCCACTTCCC	3669
Db	3343	CACCTGAAACACTGGACCTGGGGGTAGCCCCGCCAGCCCTAGTCACCCCACTTCCC	3402
QY	3670	ACTTGCACTCTTGTAGCTAGAACCTTCTCTAAGCCTATAGCTTTCGTGGAGTAAATATG	3729
Db	3403	ACTTGCACTCTTGTAGCTAGAACCTTCTCTAAGCCTATAGCTTTCGTGGAGTAAATATG	3460
QY	3730	GGATGGGGGGGAAAGAGGAGCAAGGAGCCCATAGCTTGGGGGTGGACATCTCTAGTGA	3789
Db	3461	GGATGGGGGGGAAAGAGGAGCAAGGAGCCCATAGCTTGGGGGTGGACATCTCTAGTGA	3519
QY	3790	GCTGCCACATTTGATTTTCTATATATACACTGGGGGTTGTACATTTTGGGGGAGAGACA	3849
Db	3520	GCTGCCACATTTGATTTTCTATATATACACTGGGGGTTGTACATTTTGGGGGAGAGACA	3579
QY	3850	CAGATTTTTCACATAATATATATGAGCACTAGCTTGGAGCAATTTTAATCCCTCAGTAGGC	3909
Db	3580	CAGATTTTTCACATAATATATATGAGCACTAGCTTGGAGCAATTTTAATCCCTCAGTAGGC	3637
QY	3910	AGGTAATATATAAAGGTTGAGTTTCCACAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTT	3953
Db	3638	AGGTAATATATAAAGGTTGAGTTTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTT	3681
RESULT 13			
AF026259			
LOCUS	AF026259	3659 bp	mRNA
DEFINITION	Mus musculus receptor-like tyrosine kinase (Nep) mRNA, complete cds.		
ACCESSION	AF026259		
VERSION	AF026259.1	GI:2564939	
KEYWORDS	house mouse, Mus musculus		
SOURCE	house mouse, Mus musculus		
ORGANISM	house mouse, Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus		
TITLE	Zerlin,M., Julius,M.A. and Goldfarb,M.		
JOURNAL	Nep: a novel receptor-like tyrosine kinase expressed in		
MEDLINE	proliferating neuroepithelia		
REFERENCE	Oncogene 8 (10), 2731-2739 (1993)		
AUTHORS	93309947		
	2 (bases 1 to 3659)		
	Zerlin,M., Julius,M.A. and Goldfarb,M.		



Db	1425	GC	GGCTCTCTCAGCAAGGCTTACAGACCGCGTGTGGAGAGAGAGCTGACGGTTACCTTT	1484
QY	1711	CT	GTCCCTGGGAGACACTATCCCTCATCAACAACCCCGAGTCTTAGAAGACACCCCGT	1770
Db	1485	CT	GTCCCTGGGAGACACCATCTCTCATCAACAACCCCGAGAGACCCGAGACACCCCTT	1544
QY	1771	AC	CAGAGACCCCGGCTCTGTGGAAATCCGCCCACTCCGCTCTGTGTCCCAATGGCT	1830
Db	1545	AC	CAGAGACCCCGGCTCTGGGGAGCTCCACCCCAATTCGCACTCCGTCCCAAGGCT	1604
QY	1831	CT	GGTTTCTCTCTCCAAATCCAGCCCTACCGCCCTTCTGGGCCACTTAGCCCGTCCG	1890
Db	1605	CT	GGTCTCTCTCTCCAAATCCAGCCCTACCGCCCTCTCTTCTGGGCCACTTAGCCCGTCCG	1664
QY	1891	CT	CAGAGCCCGGCGCCCGCCACACACCGCCTGGGCAAAACCCACCAACCCAGGCTACA	1950
Db	1665	CT	CAGAGCCCGGCGCCCGCCACACCGCCTGGGCAAAACCCACCAACCCAGGCTCTGCA	1724
QY	1951	GT	GGGGAATATATGAGACCTTGAAAGCCAGGCGCCCGCTTCTGCCCCCACTCCAGCA	2010
Db	1725	GT	GGGGAATATATGAGACCCGAGAAAGCGGGGTGCCCGCTCTACCCCACTCCAGCA	1784
QY	2011	ACA	CGTCCCATATATGAGAGGCTACAAATGTATACCTGCAAGGGGCTACCGGGGCA	2070
Db	1785	ACA	CGTCCCATATATGAGAGGCTACAAATGTATACCTGCAAGGGGCTACCGGGGCA	1844
QY	2071	ACA	CTATGCTGTGCTGCACTGCCCCAGGGGAGTGGGGATGGGCCCCCAGAGATGG	2130
Db	1845	ACA	CTATGCTGTGCTGCACTGCCCCAGGGGAGTGGGGATGGGCCCCCAGAGATGG	1904
QY	2131	ATT	TCCCTGCATCTCCGACTCCGCTTCAAGAGAAAGCTTGGCGAGGGCCAGTTTGGGAG	2190
Db	1905	ATT	TCCCTGCATCTCCGACTCCGCTTCAAGAGAAAGCTTGGCGAGGGCCAGTTTGGGAG	1964
QY	2191	TGC	ACTGTGTGAGTGTGACAGCCCTCAAAATCGTGGGCACTGATTTCCCTTAAATG	2250
Db	1965	TAC	ACTGTGTGAGTGTGAGAACCCCGAAGATCTGTCACTAGTACTTCCCTTAAATG	2024
QY	2251	TGC	TAAAGGACACCCCTTGTGTGTCAAGATCTTTACGGCCAGATGCCACCAAGA	2310
Db	2025	TGC	TAAAGGACACCCCTTGTGTGTCAAGATCTTTACGGCCAGATGCCACCAAGA	2084
QY	2311	AT	CCAGCTTCTCTGTCTCCAGAAATGATTTCTGAAAGAGTGAAGATCATGTGCA	2370
Db	2085	AT	CCAGCTTCTCTGTCTCCAGAAATGATTTCTGAAAGAGTGAAGATCATGTGCA	2126
QY	2371	GCG	TCAAGGACCCCAACATCATTCGGCTGTGGGCTGTGTGTGCAAGAGACCCCTCT	2430
Db	2127	GCG	TCAAGGACCCCAACATCATTCGGCTGTGGGCTGTGTGTGCAAGAGACCCCTCT	2186
QY	2431	GCA	TGATTACTGACTCAATGAGAAAGGGGACCTCAACAGTTCCTCAATGCCACCAAG	2490
Db	2187	GCA	TGATTACTGACTCAATGAGAAAGGGGACCTCAACAGTTCCTCAATGCCACCAAG	2246
QY	2491	TGG	AGACAGGACCGGAGGGGCGCTGGGGACGGGCGGCGACAGGGGCGGACCAACCA	2550
Db	2247	TGG	AGACAGGACCGGAGGGGCGCTGGGGACGGGCGGCGACAGGGGCGGACCAACCA	2306
QY	2551	TG	AGCAACCAATGCGTGCATGTGGGACCCCAATGCGCTTCGGCATGCGCTATCTGG	2610
Db	2307	TG	AGCAACCAATGCGTGCATGTGGGACCCCAATGCGCTTCGGCATGCGCTATCTGG	2366
QY	2611	CC	ACAATCTTATCTACATCGGAGACTGGACCGGAACTGCTAGTGGGGAAATTT	2670
Db	2367	CC	ACAATCTTATCTACATCGGAGACTGGACCGGAACTGCTAGTGGGGAAATTT	2426
QY	2671	TC	ACATATAAAATCCGACACTTTGGCATGAGCCGGAACCTCTATGCTGGGACTATAC	2730
Db	2427	TC	ACATATAAAATCCGACACTTTGGCATGAGCCGGAATCTCTACGCTGGGATTTATAC	2486
QY	2731	GT	GTCAAGGCGGCGAGTGGGCCATCCCTGGATGGCTGGGATGTGATCTCATGG	2790



QY	3860	CACATATATATGAGCTAGCTAGGACATTTTAATCCCTGACACAGACAGTATTAAT	3319
Db	3547	CACATATATATGAGCTAGCTAGGACATTTTAATCCCTGACACAGACAGTATTAAT	3606
QY	3920	AAAGTTGAGTTT	3933
Db	3607	AAAGTTGAGTTT	3620
RESULT	14		
MUSCASC			
LOCUS	MUSCASC	3674 bp	RNA
DEFINITION	Mus musculus Cak receptor kinase mRNA, complete cds.		31-JUL-1996
ACCESSION	L57509		
VERSION	L57509.1	GI:1161062	1
KEYWORDS	receptor kinase.		
SOURCE	Mus musculus (strain C57BL)	CDNA to mRNA.	
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 3674)		
TITLE	Perez,J.L., Jing,S.O. and Wong,T.W.		
JOURNAL	Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines		
MEDLINE	Oncogene 12 (7), 1469-1477 (1996)		
FEATURES	96204002		
Source	Location/Qualifiers		
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BASE COUNT	721 a	1090 c	1079 g
ORIGIN			784 t
Query Match	60.0%:	Score 2378.4:	DB 10; Length 3674;
Best Local Similarity	81.3%:	Pred. No. 0;	
Matches 2981:	Conservative	0; Mismatches	581; Indels 104; Gaps 15;
QY	277	AGAGATGCTGCCCCACACCCCTTAGGCCGAGGATCAGAGCTATGGACACAGAGCCC	336
Db	63	AGAGATGCTGCCCCCTTCATAGACCAGAGGGATCCAGAGCCATGGGACAGGAGACC	122
QY	337	TGTATCTTTACTCTGCTG---CTCTTGTTGGCAAGTGGAGATGCTACATGAAGGAC	393

Db	123	TCATCTCTACTGCTGCTGCTACTCTGTGACAAATTGGAGATGCTGACATGAAGGAC	182
QY	394	ATTTTGATCCGCGCCAAAGTGGCCGATATGCCCCCTGGGCAATGCAAGACCGGACCATCCAGACA	453
Db	183	ATTTTGAACCTTCCGCAAGTGGCGGCTATGCCCCGTTGGGCAATGCAAGACCGGACCATTCCTGACA	242
QY	454	GTCGATCTGCTCTCCAGCTCTGTCGATGTCATGTTCCATCGCCGCGGCAAGCAGAGSTTG	513
Db	243	GGGATATCTGTGTCCAGCTCTGTCGAGCTTACCCTGCCCCGACAGAGAGCTTG	302
QY	514	AGAGCAGTACCGGGAGTGGGCTGTGGCCCCGAGGGTCTGTTTCCAAAGAGAGG	573
Db	303	AAAGCAGTGAATGAGATGGGCTGTGGCCCCGAGGGCTGTGTTTCCAAAGAGAGG	362
QY	574	AGTACTTGCAGTGGATCTCAAGAGCATCCAGCTGGTCTGTGGTGGCACCCAGGAC	633
Db	363	ACTTACTGCAGTGGACCTTGTAGGCTACACGTGGTCTGTGGTGGCACCCAGGAG	422
QY	634	GGCATGCCCCGGGAGCTGGGCAAGAGATTTCCCGAGACTACCGGCTGCTTACTCCGGG	693
Db	423	GGCATGCTGGGGGTCCTGGGCAAAAGTTCCTCCGAACTATCGGTTGCTTACTCCGAG	482
QY	694	ATGTCCTGCCCTGGATGGGCTGGAAGGACCGCTGGGGTCAAGAGGTATCTAGGCAATG	753
Db	483	ATGGCCGCTGATGATGACTGGAAGGACCGCTGGGGACAGAGGTGATTTGGGTAACG	542
QY	754	AGGACCCGTGAAGGATGGTGTGAAGGACCTTGGGCCCCCAAGTGTGGCCGACTGTTC	813
Db	543	AGGATCCCGGGGAGATGTGTGTGAAGGACCTTGGGCCCCCAAGTGTGGCCGAGTGTTC	602
QY	814	GCTTCTACCCCCGGGCTGACCGGGTCTAGATGTCTGTCTGCGGGTGAAGACTTATGCT	873
Db	603	GCTTCTACCCCCAGGGCTGACCGGGTCTAGATGTCTGTCTGTGGTGGAGCTTATGGCT	662
QY	874	GCTCTGGAAGGATGAGACTCTGTCTTACACCGCCCTGTGGGGCAGACATGTAATTAT	933
Db	663	GCTCTGCGGGGATGAGACTCTGTCTATATACACCCCCGTGGGGCAGACATGCACTTAT	722
QY	934	CTGAG --- CCGTGTACTCTCAAGCACTCCACCTATGACGAGCATTAACGTTGGGCGGACCTG	990
Db	723	CTGAGGTGATGTATCTCAATCTCAATGATTTCCACTTACGATGATTACTGCTGGAGGGCTGC	782
QY	991	AGTATGGGGGCTGTGGGCCCACTGGCAGAGTGTGTGGGGCTGATGACTTTAGAAAG	1050
Db	783	AGTATGGGGGCTGTGGGCCCACTGGCAGAGTGTGTGGGGCTGATGACTTTCAAGCAGA	842
QY	1051	GTCAGGAGCTGCGGGGCTGGCCAGAGGCTATGACATATGGGATGGAGCAACCACTACTCT	1110
Db	843	GCCAGGAGCTGCGGGGCTGGCCAGAGGCTATGACATATGGGATGGAGCAACCACTACTCC	902
QY	1111	CCAATGCTATGTGGAATGAGTGTGATGTTTACCGCGCTGAGGGCTCCAGGCTATTC	1170
Db	903	CCAAGGCTACTGTGAGATGAGTGTGATGTTTATGCTGTTGAGGACCTTCCAGACCATGC	962
QY	1171	AGGTCCACTGTACAAATATGACACTCTGGGAGCCCGCTACCAAGTGGGGGAGTATCC	1230
Db	963	AGGTCCACTGTACAAATATGACACTCTGGGAGCCCGCTACCAAGTGGGGGAGTATCC	1022
QY	1231	GCTTCCCGGCGGCTGCGCATGAGCTGTGGAGGGGAGGACCAATGGGCCCACTATGAGG	1290
Db	1023	GCTTAAAAAGGGGTCCCGCATATGGCTGTGGAAAGGAGACTGTCCGCAATGCTCTGGAG	1082
QY	1291	GCAACTGTGGGGAACCCAGAGCCCGGAGCTGTCAATGCCCCCTTGGGCGCTGTGGCTC	1350
Db	1083	GCAACTGTGAGAACCCAGAGCCCGGAGCATCTCAATGCCCCCTTGGGAGCACGTGGGCG	1142
QY	1351	GCTTGTGCAAGTCCCGCTTCTTTTGGGGGGCGGTTACTCTTCAAGCAAAATCTCT	1410
Db	1143	GCTTGTGCAAGTCAATTCCTTTTTCAGAGTCTTGGTTACTCTTCAAGTGAATCTTT	1202
QY	1411	TCATCTCTGATGTGTGAACAATTCCTCTCGGCACTGGGAGGACCTTCCTCCAGAGCC	1470
Db	1203	TCATCTCTGATGTGTGAACAATTCCTCT --- GACACTCTCCACAGAGCC	1250



QY	1471	CTGTGGCGCGCTGGGCCACTTCCACCACTTCAGACGTTGGAGTGGAGCCACAG	1530
Db	1251	CTGTGGCGCCACCTGGCCCGGCTCCCAACCACTTCAGAGCTTGGAGTGGAGCCCGG	1310
QY	1531	GCCAGACCGCCGTGGCCCAAGGCCCAAGGGAGCCGACCGCATCTCATCGGCTGCTGG	1500
Db	1311	GTCACAGCCAGTGGCCCAAGCGGAGGGAGGCCCACTGGCATCTCATTTGGCTCTGG	1370
QY	1591	TGGCCATCATCTGCTCTGCTGTGCATCATATGGCCATATGCTCTGGCGGCTGCACGGC	1650
Db	1371	TGGCCATCATCTGCTCTGCTGTGCATCATATGCGGCTGATGCTTGGAGGCTGCACGGC	1430
QY	1651	GCAGGCTCTTCAGCAAGGCTGAAACGAGGGTGTGTGAAGAGAGACTGACGGTTCACCT	1710
Db	1431	GCCGCGCTCTCAGCAAGGCTGAGGGGTGGTGTGAAGAGAGACTGACGGTTCACCTTT	1490
QY	1711	CTGTCCCTGGGGACATCATCTCATCAACAACCGCCCAAGTCTTAGAGAGCACCCCGT	1770
Db	1491	CTGTCCCTGGGGACATCATCTCATCAACAACCGCCCAAGACCCCGAGACACACCCCTT	1550
QY	1771	ACCAGAGCCCGGCGCTCTGTGGAAATCCGCCCCACTCGCTCCCTGTATGCCCAATGGT	1830
Db	1551	ACCAGAGCCCGGCGCTCTGGGGAGCTCCACCCCATTTGTGACCTCGGTCCCAACGGCT	1610
QY	1831	CTGCGTTCGCTGCTCCATATCCAGCCTACCGCTCTTGTGGCACTTACGCGCTGCC	1890
Db	1611	CTGCGTTCGCTGCTCCAAATCCGCGCTTACCGCTCTTGTGGCACTTACGCGCTGCC	1670
QY	1891	CTGAGAGCCCGGCGCCCGCCACACCGCCGCTGGGGCAACCCACCAACACCAGGCTTACA	1950
Db	1671	CTGAGAGCCCGGCGCCCGCCACACCGCCGCTGGGGCAACCCACCAACACCAGGCTTACA	1730
QY	1951	GTCGGGACATATATGAGCCGTGAGAAAGCAAGGCCCGCGCTTCTGCCCCACTTCCACA	2010
Db	1731	GTCGGGACATATATGAGAGCCCGAGAAAGCGGGTCCCGCTTACCCCACTTCCACAGA	1790
QY	2011	ACAGCCGCCCCCAATTATGCCGAGAGCTGACATTTTACCTTCAGAGGCGCTACCGGGGCA	2070
Db	1791	ACAGCCGCCCCCAATTATGCCGAGAGCTGACATTTTACCTTCAGAGGCGCTACCGGGGCA	1850
QY	2071	ACACCTATGCTGTGCGCTGCACACTGCCCCAGGGGCACTGGGGATGGGCCCCCAAGATG	2130
Db	1851	ACACCTATGCTGTGCGCTGCACACTGCCCCAGGGGCGTTGGGGATGGGCCCCCAAGATG	1910
QY	2131	ATTTCCTCGATCTGCATCTCGCTTCAAGAGAAAGCTTGGCGAGGCCATGTTGGGAG	2190
Db	1911	ATTTCCTCGATCTGCACACTCGCTTCAAGAGAAAGCTTGGCGAGGCCATTTGGGAG	1970
QY	2191	TGCAGCTGTGTGAGGTCGACAGCGCTCAAGATCTGGTCACTGTATTTCCCCCTTAATG	2250
Db	1971	TACACTGTGTGAAGTATGAGAACCGCCCAAGATCTGGTCACTGTATTTCCCTATAGTG	2030
QY	2251	TGCGTAAGGAGCAACCTTGTGCTGTGATGCTGAAGATCTTAAGGCGCAGATGCCACAAGA	2310
Db	2031	TGCACAAGGAGCAACCCCTGTGTGTGATGCTGAAGATCTTCCGGCCAGATGCCACAAGA	2090
QY	2311	ATGCCAGCTTCTCTGTTCTCCAGGAATGATTTCTGTAAAGAGTGAAGATCATGTGCA	2370
Db	2091	ATG-----CCAGGAATGATTTCTGTAAAGAGTGAAGATCATGTGCA	2132
QY	2371	GGCTCAAGGACCCCAACATCATTTGCGGCTGCTGGCGTGTGTGACGAGCAAGCCCTGT	2430
Db	2133	GGCTCAAGGACCCCAACATCATTCGGGCTCTGGGTGTGTGTGACGAGTGAACCCCTGT	2192
QY	2431	GCATGATTAATCTATCATATGAGAAAGCGGACCTCAACCAAGTTCTCTCAATGCCACAC	2490
Db	2193	GCATGATTAATCAATCAATATGAGAAAGCGGATCTCAACCAAGTTCTCTCAATGCCACAC	2252
QY	2491	TGGAGAGCAAGGACCAAGGAGGGGCGCTGGGGAGAGGGGAGGCTGCAAGGGGCCACACA	2550
Db	2253	TGGAAACAAAGGCACTCAAGGGGCTCTGTGGGGACACAGAGTCTCAACCAAGGGGCCACACA	2312

QY	2551	TCAGCTACCCAATGCTGCTGCATGTGGCAGCCAGATGCGCTCGGCATGCGCTATCTGG	261
Db	2313	TCAGCTACCCATGCTGTTTACACGTGGGGGGCCCAATGCGCTCTGGCATTGCTTATCTGG	237
QY	2611	CCACACCTAACTTTGTACATGGGACCTGGCCACCGGAACTGCTTACTGGGGAAATTT	267
Db	2373	CCAGCGTAACCTTTGTGATCGGGGACCTGGCCACCGGAAACGCTTGGTTGGGGAAATTT	243
QY	2671	TCACCACTAAATGCGACACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTTTTACC	273
Db	2433	TCACCACTAAATGCGCGACTTTGGCATGAGCCGGAATCTTACGCTGGGGATTTTATACC	249
QY	2731	GTGTGCAGAGGCCGGGACAGTGCCTGCCCATCGCTGGATGGAGCTCGGGAGTGCATCTCATGG	279
Db	2493	GTGTGCAGAGGCCGGGGCGGTGCTGCCCATCAGGTGGATGGCTTGGGAGTGCATCTCATGG	255
QY	2791	GGAAGTTCACACACTGCGAGTACGTGTGGCCCTTTGGTGTACCTGTGGGAGTGTCTGA	285
Db	2553	GGAAGTTCACAAACAGCCAGTACGTTTGGGCGCTTGGAGTGCACCTGTGGGAGTGTCTGA	261
QY	2851	TGCTCTGAGGGGCCAGCGCCCTTTGGGACGCTCACCGAGACAGGTCACTCGAAGACGGG	291
Db	2613	TGCTCTGAGGTCCCAAGCCCTTTGGGACGCTTACAGATGACAGGTATTCGAAGATGGCG	267
QY	2911	GGGAGTTCCTCCGGGACAGAGGCGCGCAGGTACCTCTCCCGGCGCGCTGCTCTCCGCG	297
Db	2673	GGGAGTTCCTTCCAGGACAGAGGCGCGCAGGTCTACTTTCAGAGCCACCCGCTCTCCAC	273
QY	2971	AGGGCGTAATAGACTATGCTTGGTGTGGAGCCGGGAGTCTTGACAGGACGACCCCT	303
Db	2733	AGAGCCCTGTAATGACTATGCTCGGHTGTGGAGCCGGGAGCCGAGCAGGGCGCGCCT	279
QY	3031	TTTCCCGAGCGCACTGGGTTCTCTGGCAGAGATGCACTAACACGCTGTGAATCACATCT	309
Db	2793	TGCGCCAGCTTCATCGGTTCTTGGCGGATGATGGCTTCMACAGGTGTAAACTCGAGACC	285
QY	3091	CAGCTGCCCCCTCCCTCAGGAGTATCAGGGGGAAGCCAGTACACTAAACAAGAGAGAC	315
Db	2853	CGGCAAGCCCTTTCCCAATGGAAGGCCATCCAGGGGAAAGCTGGACTCGAANAAC -CGAGAGA	2911
QY	3151	ACAATGGCACCTTGCCCTTCCCTTCCCGAGAGCCATCACCTCTAATAGAGGACGATGAG	321
Db	2912	CTATGGGACCGGACCCACCCAGCTCTCATACTTGCC -CATTTCCCAAGAGGTCAGTCTC	296
QY	3211	ACTGCAAGTGGGCTGGGGCCACCCAGGGAGCTGATGCCCTTCTCCCTCTTGACACGA	327
Db	2970	TCGTGAGGGGTTATGGCTGGGACTGGGACTGCCAAGG - - - - -AATCAGA	3012
QY	3271	CTCTCATGTCCTCCCTCTCTCTTCTTCTTCCATAGAAAGCCCTGTGCGCCACCCACTGCTC	333
Db	3013	TTTACACACACTCTTTCAGTTTCTTCTTCTTCATCTGCGCAAGTGCACCCCTCCCACTGGCC	307
QY	3331	CTGTGATGGGATCTCTCCACCCCTCTCTTAGCCATCCTTTGGGGAAGGGTGGGGAGAA	339
Db	3073	CTGTGATGGGATCTGCTGCTGACTTCTTCCAGCATCCCTTGGGGAAGAACGGGGGCAAA	313
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LOCUS Rattus norvegicus tyrosine kinase receptor (Ptk-3) gene, complete cds.
DEFINITION L26525.1 GI:432480
VERSION tyrosine kinase receptor.
KEYWORDS Rattus norvegicus strain Sprague-Dawley DNA.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 3743)
AUTHORS Sanchez,M.P., Tapley,P., Salni,S.S., He,B., Pulido,D. and Batdacid,M.
TITLE Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Ptk-3, a receptor expressed in proliferative zones of the developing brain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (5), 1819-1823 (1994)
MEDLINE 94173920
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